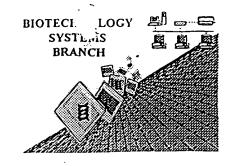# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/844,564_

Source: _OIPE_

Date Processed by STIC: _7/20/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   **SERIAL NUMBER:** 09/899,569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
       Wrapped Aminos ·   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                          prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
       Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                           ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                           each n or Xaa can only represent a single residue. Please present the maximum number of each
                           residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
       "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                           previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                           the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                           Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
       (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                           (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                           (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                           This sequence is intentionally skipped

                           Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
       (NEW RULES)   <210> sequence id number
                           <400> sequence id number
                           000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
       (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                           In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
        Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                           is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                           Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                           "Unknown." Please explain source of genetic material in <220> to <223> section.
                           (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
        "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                           listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

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          RAW SEQUENCE LISTING              DATE: 07/20/2001
          PATENT APPLICATION:  US/09/899,569     TIME: 14:20:30

          Input Set : A:\0652 2280001 seq list.txt
          Output Set: N:\CRF3\07202001\I899569.raw
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Does Not Comply
Corrected Diskette Needed
See Add 1

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   4 <110> APPLICANT: Schweifer, Norbert
   5         Scherl-Mostageer, Marwa
   6         Sommergruber, Wolfgang
   7         Abseher, Roger
   9 <120> TITLE OF INVENTION: Tumorassoziiertes Antigen (B345)
  11 <130> FILE REFERENCE: 0652.2280001/EKS/AES
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/899,569
C--> 14 <141> CURRENT FILING DATE: 2001-07-06
  16 <150> PRIOR APPLICATION NUMBER: DE 100 33 080.0
  17 <151> PRIOR FILING DATE: 2000-07-07
  19 <150> PRIOR APPLICATION NUMBER: DE 101 19 294.0
  20 <151> PRIOR FILING DATE: 2001-04-19
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  23 <151> PRIOR FILING DATE: 2000-10-25
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  34 <210> SEQ ID NO: 1
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  36 <212> TYPE: DNA
  37 <213> ORGANISM: Homo sapiens
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  41 <222> LOCATION: (1)..(214)
  43 <220> FEATURE:
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  45 <222> LOCATION: (215)..(2464)
  47 <220> FEATURE:
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  49 <222> LOCATION: (2465)..(5897)
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  56  acgagaaagc aacattacag ttctcataaa gctggggacc ccgactctgc tggcaaaacc 180
  58  ctgttacatc gtcatttcta aaagacatat aacc atg ttg tcc atc aag tct gga 235
  59                                        Met Leu Ser Ile Lys Ser Gly
  60                                        1               5
  62  gaa aga ata gtc ttt acc ttt agc tgc cag agt cct gag aat cac ttt 283
  63  Glu Arg Ile Val Phe Thr Phe Ser Cys Gln Ser Pro Glu Asn His Phe
  64          10              15                  20
  66  gtc ata gag atc cag aaa aat att gac tgt atg tca ggc cca tgt cct 331
  67  Val Ile Glu Ile Gln Lys Asn Ile Asp Cys Met Ser Gly Pro Cys Pro
  68          25              30                  35
  70  ttt ggg gag gtt cag ctt cag ccc tcg aca tcg ttg ttg cct acc ctc 379
  71  Phe Gly Glu Val Gln Leu Gln Pro Ser Thr Ser Leu Leu Pro Thr Leu
  72  40              45              50                  55
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77                   60                  65                  70
79   gag ctg cag ttt tcc atc cct cgc ctg agg cag atc ggt ccg ggt gag   475
80   Glu Leu Gln Phe Ser Ile Pro Arg Leu Arg Gln Ile Gly Pro Gly Glu
81                   75                  80                  85
83   agc tgc cca gac gga gtc act cac tcc atc agc ggc cga atc gat gcc   523
84   Ser Cys Pro Asp Gly Val Thr His Ser Ile Ser Gly Arg Ile Asp Ala
85                   90                  95                  100
87   acc gtg gtc agg atc gga acc ttc tgc agc aat ggc act gtg tcc cgg   571
88   Thr Val Val Arg Ile Gly Thr Phe Cys Ser Asn Gly Thr Val Ser Arg
89        105                 110                 115
91   atc aag atg caa gaa gga gtg aaa atg gcc tta cac ctc cca tgg ttc   619
92   Ile Lys Met Gln Glu Gly Val Lys Met Ala Leu His Leu Pro Trp Phe
93   120                 125                 130                 135
95   cac ccc aga aat gtc tcc ggc ttc agc att gca aac cgc tca tct ata   667
96   His Pro Arg Asn Val Ser Gly Phe Ser Ile Ala Asn Arg Ser Ser Ile
97                   140                 145                 150
99   aaa cgt ctg tgc atc atc gag tct gtg ttt gag ggt gaa ggc tca gca   715
100  Lys Arg Leu Cys Ile Ile Glu Ser Val Phe Glu Gly Glu Gly Ser Ala
101                  155                 160                 165
103  acc ctg atg tct gcc aac tac cca gaa ggc ttc cct gag gat gag ctc   763
104  Thr Leu Met Ser Ala Asn Tyr Pro Glu Gly Phe Pro Glu Asp Glu Leu
105                  170                 175                 180
107  atg acg tgg cag ttt gtc gtt cct gca cac ctg cgg gcc agc gtc tcc   811
108  Met Thr Trp Gln Phe Val Val Pro Ala His Leu Arg Ala Ser Val Ser
109       185                 190                 195
111  ttc ctc aac ttc aac ctc tcc aac tgt gag agg aag gag gag cgg gtt   859
112  Phe Leu Asn Phe Asn Leu Ser Asn Cys Glu Arg Lys Glu Glu Arg Val
113  200                 205                 210                 215
115  gaa tac tac atc ccg ggc tcc acc acc aac ccc gag gtg ttc aag ctg   907
116  Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro Glu Val Phe Lys Leu
117                  220                 225                 230
119  gag gac aag cag cct ggg aac atg gcg ggg aac ttc aac ctc tct ctg   955
120  Glu Asp Lys Gln Pro Gly Asn Met Ala Gly Asn Phe Asn Leu Ser Leu
121                  235                 240                 245
123  caa ggc tgt gac caa gat gcc caa agt cca ggg atc ctc cgg ctg cag   1003
124  Gln Gly Cys Asp Gln Asp Ala Gln Ser Pro Gly Ile Leu Arg Leu Gln
125                  250                 255                 260
127  ttc caa gtt ttg gtc caa cat cca caa aat gaa agc aat aaa atc tac   1051
128  Phe Gln Val Leu Val Gln His Pro Gln Asn Glu Ser Asn Lys Ile Tyr
129       265                 270                 275
133  gtg gtt gac ttg agt aat gag cga gcc atg tca ctc acc atc gag cca   1099
134  Val Val Asp Leu Ser Asn Glu Arg Ala Met Ser Leu Thr Ile Glu Pro
135  280                 285                 290                 295
137  cgg ccc gtc aaa cag agc cgc aag ttt gtc cct ggc tgt ttc gtg tgt   1147
138  Arg Pro Val Lys Gln Ser Arg Lys Phe Val Pro Gly Cys Phe Val Cys
139                  300                 305                 310
142  cta gaa tct cgg acc tgc agt agc aac ctc acc ctg aca tct ggc tcc   1195
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143  Leu Glu Ser Arg Thr Cys Ser Ser Asn Leu Thr Leu Thr Ser Gly Ser
144              315             320             325
146  aaa cac aaa atc tcc ttc ctt tgt gat gat ctg aca cgt ctg tgg atg   1243
147  Lys His Lys Ile Ser Phe Leu Cys Asp Asp Leu Thr Arg Leu Trp Met
148              330             335             340
150  aat gtg gaa aaa acc ata agc tgc aca gac cac cgg tac tgc caa agg   1291
151  Asn Val Glu Lys Thr Ile Ser Cys Thr Asp His Arg Tyr Cys Gln Arg
152          345             350             355
154  aaa tcc tac tca ctc cag gtg ccc agt gac atc ctc cac ctg cct gtg   1339
155  Lys Ser Tyr Ser Leu Gln Val Pro Ser Asp Ile Leu His Leu Pro Val
156  360             365             370             375
158  gag ctg cat gac ttc tcc tgg aag ctg ctg gtg ccc aag gac agg ctc   1387
159  Glu Leu His Asp Phe Ser Trp Lys Leu Leu Val Pro Lys Asp Arg Leu
160              380             385             390
162  agc ctg gtg ctg gtg cca gcc cag aag ctg cag cag cat aca cac gag   1435
163  Ser Leu Val Leu Val Pro Ala Gln Lys Leu Gln Gln His Thr His Glu
164              395             400             405
166  aag ccc tgc aac acc agc ttc agc tac ctc gtg gcc agt gcc ata ccc   1483
167  Lys Pro Cys Asn Thr Ser Phe Ser Tyr Leu Val Ala Ser Ala Ile Pro
168              410             415             420
170  agc cag gac ctg tac ttc ggc tcc ttc tgc ccg gga ggc tct atc aag   1531
171  Ser Gln Asp Leu Tyr Phe Gly Ser Phe Cys Pro Gly Gly Ser Ile Lys
172          425             430             435
174  cag atc cag gtg aag cag aac atc tcg gtg acc ctt cgc acc ttt gcc   1579
175  Gln Ile Gln Val Lys Gln Asn Ile Ser Val Thr Leu Arg Thr Phe Ala
176  440             445             450             455
178  ccc agc ttc caa caa gag gcc tcc agg cag ggt ctg acg gtg tcc ttt   1627
179  Pro Ser Phe Gln Gln Glu Ala Ser Arg Gln Gly Leu Thr Val Ser Phe
180              460             465             470
182  ata cct tat ttc aaa gag gaa ggc gtt ttc acg gtg acc cct gac aca   1675
183  Ile Pro Tyr Phe Lys Glu Glu Gly Val Phe Thr Val Thr Pro Asp Thr
184              475             480             485
186  aaa agc aag gtc tac ctg agg acc ccc aac tgg gac cgg ggc ctg cca   1723
187  Lys Ser Lys Val Tyr Leu Arg Thr Pro Asn Trp Asp Arg Gly Leu Pro
188              490             495             500
191  tcc ctc acc tct gtg tcc tgg aac atc agc gtg ccc aga gac cag gtg   1771
192  Ser Leu Thr Ser Val Ser Trp Asn Ile Ser Val Pro Arg Asp Gln Val
193          505             510             515
195  gcc tgc ctg act ttc ttt aag gag cgg agc ggc gtg gtc tgc cag aca   1819
196  Ala Cys Leu Thr Phe Phe Lys Glu Arg Ser Gly Val Val Cys Gln Thr
197  520             525             530             535
199  ggg cgc gca ttc atg atc atc cag gag cag cgg acc cgg gct gag gag   1867
200  Gly Arg Ala Phe Met Ile Ile Gln Glu Gln Arg Thr Arg Ala Glu Glu
201              540             545             550
203  atc ttc agc ctg gac gag gat gtg ctc ccc aag cca agc ttc cac cat   1915
204  Ile Phe Ser Leu Asp Glu Asp Val Leu Pro Lys Pro Ser Phe His His
205              555             560             565
207  cac agc ttc tgg gtc aac atc tct aac tgc agc ccc acg agc ggc aag   1963
208  His Ser Phe Trp Val Asn Ile Ser Asn Cys Ser Pro Thr Ser Gly Lys
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PATENT APPLICATION: US/09/899,569   TIME: 14:20:30

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215   ttg act gtc atc ctc atc gca gcg gtg gga ggt gga gtc tta ctg ctg   2059
216   Leu Thr Val Ile Leu Ile Ala Ala Val Gly Gly Gly Val Leu Leu Leu
217   600                 605                 610                 615
219   tct gcc ctc ggg ctc atc att tgc tgt gtg aaa aag aag aaa aag aag   2107
220   Ser Ala Leu Gly Leu Ile Ile Cys Cys Val Lys Lys Lys Lys Lys Lys
221                      620                 625                 630
223   aca aac aag ggc ccc gct gtg ggt atc tac aat ggc aac atc aat act   2155
224   Thr Asn Lys Gly Pro Ala Val Gly Ile Tyr Asn Gly Asn Ile Asn Thr
225                      635                 640                 645
227   gag atg cca ggc agc caa aaa agt ttc aga aag ggc gaa agg aca atg   2203
228   Glu Met Pro Gly Ser Gln Lys Ser Phe Arg Lys Gly Glu Arg Thr Met
229          650                 655                 660
231   act ccc atg tgt atg cag tca tcg agg aca cca tgg tat atg ggc atc   2251
232   Thr Pro Met Cys Met Gln Ser Ser Arg Thr Pro Trp Tyr Met Gly Ile
233          665                 670                 675
235   tgc tac agg att cca gcg gct cct tcc tgc agc cag agg tgg aca cct   2299
236   Cys Tyr Arg Ile Pro Ala Ala Pro Ser Cys Ser Gln Arg Trp Thr Pro
237   680                 685                 690                 695
239   acc ggc cgt tcc agg gca cca tgg ggg tct gtc ctc cct ccc cac cca   2347
240   Thr Gly Arg Ser Arg Ala Pro Trp Gly Ser Val Leu Pro Pro His Pro
241                      700                 705                 710
243   cca tat gct cca ggg ccc caa ctg caa agt tgg cca ctg agg agc cac   2395
244   Pro Tyr Ala Pro Gly Pro Gln Leu Gln Ser Trp Pro Leu Arg Ser His
245                      715                 720                 725
249   ctc ctc gct ccc ctc ctg agt ctg aga gtg aac cgt aca cct tct ccc   2443
250   Leu Leu Ala Pro Leu Leu Ser Leu Arg Val Asn Arg Thr Pro Ser Pro
251          730                 735                 740
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361  tgtgctttaa ataaacaaat gtaccaaaaa acaagtatca agctgtttaa gtgcttcggc 5674
363  tacttgtccc ctggttcagt agaggccccg gtttcccagt tgttgactgt gacaggctca 5734
365  gcatgggctc agcagatgct gtcttaattt gtggatgata cagaaagcca ggctttggga 5794
367  tacaagttct ttcctcttca tttgatgccg tgcactgtgt gaagcagatg tttttgtccg 5854
369  gaaataaaaa taatagtctt ggagtctcgc caaaaaaaaa aag              5897
373  <210> SEQ ID NO: 2
374  <211> LENGTH: 749
375  <212> TYPE: PRT
376  <213> ORGANISM: Homo sapiens
378  <400> SEQUENCE: 2
379  Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe Ser Cys
380    1              5              10              15
```

See item number 9 on ERROR Summary Sheet

```
<210> 38
<211> 23
<212> DNA
<213> Kunstliche Sequenz

<220>
<221> 5'UTR
<222> (1)..(282)

<220>
<221> GC_signal
<222> (147)..(157)

<220>
<221> misc_feature
<222> (201)..(209)
<223> cap signal; Transkriptionsstart

<220>
<221> 3'UTR
<222> (2794)..(6163)

<220>
<221> 3'UTR
<222> (2794)..(6163)

<220>
<221> CDS
<222> (283)..(2793)

<400> 38
agcagcagaa cccctagcag tgc                                        23
```

The ranges provided for numeric identifier <222> are larger than the actual sequence.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/899,569

DATE: 07/20/2001
TIME: 14:20:31

Input Set : A:\0652 2280001 seq list.txt
Output Set: N:\CRF3\07202001\I899569.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:351 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:353 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:355 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1500 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 5UTR LOCATION: (1)..
(282)
L:1513 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 3UTR LOCATION:
(2794)..(6163)
L:1517 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 3UTR LOCATION:
(2794)..(6163)
L:1521 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, CDS LOCATION: (283)..
(2793)